**Copper ion altered association network among multi-genes and enzyme activity of laccase in *Ganoderma lucidum***

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**Table S1 Primer pairs designed for qPCR analysis**

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Forward** | **Reverse** | **Amplicon length(bp)** |
| *Lacc1* | CCATTCGCTCACCGTCATC | CCTTTGCCTTCGTTGTTGTTC | 165 |
| *Lacc2* | GTTCCTCCACTGCCACATC | CAGAGTTCCTTCCACGAGTC | 117 |
| *Lacc3* | CTTACGGGAAACAAGGGTGAT | TGGAGTGAGGTGGACTTTAGCA | 86 |
| *Lacc4* | TGTGAGCGTTGGCGATGA | CGATGTGGCAATGGAGGAAC | 189 |
| *Lacc5* | ATGCGGTCGTGGTCAATAG | ATGGTGTGGTTCGTCAAGTT | 103 |
| *Lacc6* | CCGCTCATCACAGGGAATAA | CACCGTCCGCCCAGTTC | 136 |
| *Lacc7* | ACGCAAGGCAAACGCTATC | GGCGGTGAGGACAAATGAG | 180 |
| *Lacc8* | TTCACTGGCACGGCTTCT | CGCTGGCAATAGGACACTG | 81 |
| *Lacc9* | AGACGCCCTTCAACATCAAC | GAGACCATACACGCTACCT | 123 |
| *Lacc10* | AGACCGACCTCCATCCTTAC | ATGAAGAAGTCCGTAGTGTTGAAG | 112 |
| *Lacc11* | ATAAGGAGGCGAAGAACACAAC | GGCGACACGGATGAATGAG | 125 |
| *Lacc12* | GCAACGACACTTCATCCAACT | AGGTGACGGAGGAGGTTATG | 105 |
| *Lacc13* | GACAACTTGAGCAATGACACCAT | TGACCATAGCAGGACCATCG | 100 |
| *Lacc14* | TCTGCCTGGTCCGCTTAT | CATCGTGTGGTTCGTGAGTT | 82 |
| *Lacc15* | CAAGCGGTGGACAACTACTG | GTAACGCAGAATCGCAGAGT | 99 |
| *Lacc16* | GCGTGATGTCGTGAACCTT | GATGAGGCAGTGGAGGAAC | 94 |
| *GAPDH* | CGCTCAACAAGAACTTCGTCAA | CGTAGACAAGGAGGTCACAGA | 87 |

**Fig. S1** Time course transcriptional profiles of putative laccase genes in *G. lucidum*. **A)** Transcriptional level of laccase genes at developmental time points under the control condition. **B)** Transcriptional level of laccase genes at developmental time points under Cu2+ stress. Transcript amounts were normalized with the endogenous reference gene *GAPDH* and calculated by 2-△CT, △CT was calculated as (CT target -CT *GAPDH*). The laccase mRNA transcript levels on the 2nd day were absent for the two groups due to insufficient amount of RNA in any type of fungal cultures.

**Fig. S2** Distribution of putative *cis*-acting elements in the promoter region of gene *Lacc1*-*Lacc16* upstream 2000 bp of the start codon. CAAT box（ ）; MRE （ ）; STRE （ ）; CRE（ ）; NIT（ ）; TATA box（ ）; XRE（ ）; ARE（ ）. MRE: Metal responsive element; STRE: stress response element; CRE: cyclic AMP-responsive element; NIT: Nitrogen repression response element; XRE: Xenobiotic response element; ARE: antioxidant responsive element.

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